RAW SEQUENCE LISTING PATENT APPLICATION US/08/842,827

TEAM 8

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DATE: 09/11/97

TIME: 11:39:07

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This Raw Listing contains the General Information Section and up to the first 5 pages.

ENTERED SEQUENCE LISTING 1 2 RECEIVED 3 (1) General Information: 4 SEP 2 5 1997 (i) APPLICANT: LEUNG, David W. 5 6 TOMPKINS, Christopher K. GROUP 1800 7 (ii) TITLE OF INVENTION: HUMAN PHOSPHATIDIC ACID PHOSPHATASE 8 9 10 (iii) NUMBER OF SEQUENCES: 21 11 12 (iv) CORRESPONDENCE ADDRESS: 13 (A) ADDRESSEE: Foley & Lardner (B) STREET: 3000 K Street, N.W., Suite 500 14 (C) CITY: Washington 15 (D) STATE: D.C. 16 (E) COUNTRY: USA 17 18 (F) ZIP: 20007-5109 19 (v) COMPUTER READABLE FORM: 20 (A) MEDIUM TYPE: Floppy disk 21 (B) COMPUTER: IBM PC compatible 22 (C) OPERATING SYSTEM: PC-DOS/MS-DOS 23 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 24 25 26 (vi) CURRENT APPLICATION DATA: (A) APPLICATION NUMBER: US 08/842,827 27 (B) FILING DATE: 17-APR-1997 28 29 (C) CLASSIFICATION: 30 (viii) ATTORNEY/AGENT INFORMATION: 31 (A) NAME: BENT, Stephen A. 32 (B) REGISTRATION NUMBER: 29,768 33 (C) REFERENCE/DOCKET NUMBER: 77319/125 34 35 (ix) TELECOMMUNICATION INFORMATION: 36 37 (A) TELEPHONE: (202)672-5300 38 (B) TELEFAX: (202)672-5399 39 (C) TELEX: 904136 40 41 42 (2) INFORMATION FOR SEQ ID NO:1: 43

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid

(A) LENGTH: 1563 base pairs

44

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RAW SEQUENCE LISTING PATENT APPLICATION US/08/842,827

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73 74	CCTCATT	CCA '	TCGC	CCTT	GC C	3GGC	AGCC	C GG	GCAG.	AGAC						353
74	CCTCATT	CCA '	TCGC	CCTT	GC CC	3GGC	AGCC	C GG(GCAG	AGAC			TT G			353
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74 75 76 77	ACG CGG	CTG	CCG	TAC	GTG	GCC	стс	GAT	GTG	CTC	Me TGC	et Pi 1 GTG	he A: TTG	sp Ly CTG	/s GCT	
74 75 76 77 78	ACG CGG	CTG	CCG	TAC	GTG Val	GCC	стс	GAT	GTG	CTC Leu	Me TGC	et Pi 1 GTG	he A: TTG	sp Ly CTG	gct Ala	
74 75 76 77 78 79	ACG CGG Thr Arg 5	CTG Leu CCT	CCG Pro	TAC Tyr GCA	GTG Val 10	GCC Ala CTT	CTC Leu ACT	GAT Asp TCA	GTG Val	CTC Leu 15 CAT	TGC Cys	et Pi 1 GTG Val	ne A: TTG Leu TTC	CTG Leu CAA	GCT Ala 20 CGA	
74 75 76 77 78 79 80	ACG CGG Thr Arg	CTG Leu CCT	CCG Pro	TAC Tyr GCA	GTG Val 10	GCC Ala CTT	CTC Leu ACT	GAT Asp TCA	GTG Val	CTC Leu 15 CAT	TGC Cys	et Pi 1 GTG Val	ne A: TTG Leu TTC	CTG Leu CAA Gln	GCT Ala 20 CGA	401
74 75 76 77 78 79 80 81 82 83	ACG CGG Thr Arg 5	CTG Leu CCT	CCG Pro	TAC Tyr GCA	GTG Val 10	GCC Ala CTT	CTC Leu ACT	GAT Asp TCA	GTG Val	CTC Leu 15 CAT	TGC Cys	et Pi 1 GTG Val	ne A: TTG Leu TTC	CTG Leu CAA	GCT Ala 20 CGA	401
74 75 76 77 78 79 80 81 82 83 84	ACG CGG Thr Arg 5 GGA TTG Gly Leu	CTG Leu CCT Pro	CCG Pro TTT Phe	TAC Tyr GCA Ala 25	GTG Val 10 ATT Ile	GCC Ala CTT Leu	CTC Leu ACT Thr	GAT Asp TCA Ser	GTG Val AGG Arg 30	CTC Leu 15 CAT His	TGC Cys ACC Thr	et Pi 1 GTG Val CCC Pro	TTG Leu TTC Phe	CTG Leu CAA Gln 35	GCT Ala 20 CGA Arg	401 449
74 75 76 77 78 79 80 81 82 83 84 85	ACG CGG Thr Arg 5 GGA TTG Gly Leu GGA GTA	CTG Leu CCT Pro	CCG Pro TTT Phe	TAC Tyr GCA Ala 25	GTG Val 10 ATT Ile	GCC Ala CTT Leu	CTC Leu ACT Thr	GAT Asp TCA Ser	GTG Val AGG Arg 30	CTC Leu 15 CAT His	TGC Cys ACC Thr	et Pi 1 GTG Val CCC Pro	TTG Leu TTC Phe	CTG Leu CAA Gln 35	GCT Ala 20 CGA Arg	401
74 75 76 77 78 79 80 81 82 83 84 85	ACG CGG Thr Arg 5 GGA TTG Gly Leu	CTG Leu CCT Pro	CCG Pro TTT Phe TGT Cys	TAC Tyr GCA Ala 25	GTG Val 10 ATT Ile	GCC Ala CTT Leu	CTC Leu ACT Thr	GAT Asp TCA Ser ATC	GTG Val AGG Arg 30	CTC Leu 15 CAT His	TGC Cys ACC Thr	et Pi 1 GTG Val CCC Pro	TTG Leu TTC Phe AAA Lys	CTG Leu CAA Gln 35	GCT Ala 20 CGA Arg	401 449
74 75 76 77 78 79 80 81 82 83 84 85 86	ACG CGG Thr Arg 5 GGA TTG Gly Leu GGA GTA	CTG Leu CCT Pro	CCG Pro TTT Phe	TAC Tyr GCA Ala 25	GTG Val 10 ATT Ile	GCC Ala CTT Leu	CTC Leu ACT Thr	GAT Asp TCA Ser	GTG Val AGG Arg 30	CTC Leu 15 CAT His	TGC Cys ACC Thr	et Pi 1 GTG Val CCC Pro	TTG Leu TTC Phe	CTG Leu CAA Gln 35	GCT Ala 20 CGA Arg	401 449
74 75 76 77 78 79 80 81 82 83 84 85 86 87 88	ACG CGG Thr Arg 5 GGA TTG Gly Leu GGA GTA Gly Val	CTG Leu CCT Pro	CCG Pro TTT Phe TGT Cys 40	TAC Tyr GCA Ala 25 AAT Asn	GTG Val 10 ATT Ile GAT Asp	GCC Ala CTT Leu GAG Glu	CTC Leu ACT Thr TCC Ser	GAT Asp TCA ser ATC Ile 45	GTG Val AGG Arg 30 AAG Lys	CTC Leu 15 CAT His	TGC Cys ACC Thr	GTG Val CCC Pro	TTG Leu TTC Phe AAA Lys	CTG Leu CAA Gln 35 GAA Glu	GCT Ala 20 CGA Arg GAC Asp	401 449 497
74 75 76 77 78 79 80 81 82 83 84 85 86 87 88	ACG CGG Thr Arg 5 GGA TTG Gly Leu GGA GTA Gly Val	CTG Leu CCT Pro TTC Phe	CCG Pro TTT Phe TGT Cys 40	TAC Tyr GCA Ala 25 AAT Asn	GTG Val 10 ATT Ile GAT Asp	GCC Ala CTT Leu GAG Glu	CTC Leu ACT Thr TCC Ser	GAT Asp TCA Ser ATC Ile 45	GTG Val AGG Arg 30 AAG Lys	CTC Leu 15 CAT His TAC Tyr	TGC Cys ACC Thr CCT Pro	et Pl 1 GTG Val CCC Pro TAC Tyr	TTG Leu TTC Phe AAA Lys 50	CTG Leu CAA Gln 35 GAA Glu	GCT Ala 20 CGA Arg GAC Asp	401 449
74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89	ACG CGG Thr Arg 5 GGA TTG Gly Leu GGA GTA Gly Val	CTG Leu CCT Pro TTC Phe	CCG Pro TTT Phe TGT Cys 40	TAC Tyr GCA Ala 25 AAT Asn	GTG Val 10 ATT Ile GAT Asp	GCC Ala CTT Leu GAG Glu	CTC Leu ACT Thr TCC Ser	GAT Asp TCA Ser ATC Ile 45	GTG Val AGG Arg 30 AAG Lys	CTC Leu 15 CAT His TAC Tyr	TGC Cys ACC Thr CCT Pro	et Pl 1 GTG Val CCC Pro TAC Tyr CCA Pro	TTG Leu TTC Phe AAA Lys 50	CTG Leu CAA Gln 35 GAA Glu	GCT Ala 20 CGA Arg GAC Asp	401 449 497
74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90	ACG CGG Thr Arg 5 GGA TTG Gly Leu GGA GTA Gly Val	CTG Leu CCT Pro TTC Phe	CCG Pro TTT Phe TGT Cys 40	TAC Tyr GCA Ala 25 AAT Asn	GTG Val 10 ATT Ile GAT Asp	GCC Ala CTT Leu GAG Glu	CTC Leu ACT Thr TCC Ser	GAT Asp TCA Ser ATC Ile 45	GTG Val AGG Arg 30 AAG Lys	CTC Leu 15 CAT His TAC Tyr	TGC Cys ACC Thr CCT Pro	et Pl 1 GTG Val CCC Pro TAC Tyr	TTG Leu TTC Phe AAA Lys 50	CTG Leu CAA Gln 35 GAA Glu	GCT Ala 20 CGA Arg GAC Asp	401 449 497
74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91	ACG CGG Thr Arg 5 GGA TTG Gly Leu GGA GTA Gly Val ACC ATA Thr Ile	CTG Leu CCT Pro TTC Phe	CCG Pro TTT Phe TGT Cys 40 TAT Tyr	TAC Tyr GCA Ala 25 AAT Asn GCG Ala	GTG Val 10 ATT Ile GAT Asp	GCC Ala CTT Leu GAG Glu TTA Leu	CTC Leu ACT Thr TCC Ser GGT Gly 60	GAT Asp TCA Ser ATC Ile 45 GGA Gly	GTG Val AGG Arg 30 AAG Lys ATA Ile	CTC Leu 15 CAT His TAC Tyr	TGC Cys ACC Thr CCT Pro	GTG Val CCC Pro TAC Tyr CCA Pro 65	TTG Leu TTC Phe AAA Lys 50 TTC	CTG Leu CAA Gln 35 GAA Glu AGT Ser	GCT Ala 20 CGA Arg GAC Asp	401 449 497 545
74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93	ACG CGG Thr Arg 5 GGA TTG Gly Leu GGA GTA Gly Val ACC ATA Thr Ile	CTG Leu CCT Pro TTC Phe CCT Pro 55	CCG Pro TTT Phe TGT Cys 40 TAT Tyr	TAC Tyr GCA Ala 25 AAT Asn GCG Ala	GTG Val 10 ATT Ile GAT Asp TTA Leu	GCC Ala CTT Leu GAG Glu TTA Leu	CTC Leu ACT Thr TCC Ser GGT Gly 60	GAT Asp TCA Ser ATC Ile 45 GGA Gly	GTG Val AGG Arg 30 AAG Lys ATA Ile	CTC Leu 15 CAT His TAC Tyr	TGC Cys ACC Thr CCT Pro ATT Ile	et Pl 1 GTG Val CCC Pro TAC Tyr CCA Pro 65	TTG Leu TTC Phe AAA Lys 50 TTC Phe	CTG Leu CAA Gln 35 GAA Glu AGT Ser	GCT Ala 20 CGA Arg GAC Asp ATT Ile	401 449 497
74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93	ACG CGG Thr Arg 5 GGA TTG Gly Leu GGA GTA Gly Val ACC ATA Thr Ile ATC GTT Ile Val	CTG Leu CCT Pro TTC Phe CCT Pro 55	CCG Pro TTT Phe TGT Cys 40 TAT Tyr	TAC Tyr GCA Ala 25 AAT Asn GCG Ala	GTG Val 10 ATT Ile GAT Asp TTA Leu	GCC Ala CTT Leu GAG Glu TTA Leu	CTC Leu ACT Thr TCC Ser GGT Gly 60	GAT Asp TCA Ser ATC Ile 45 GGA Gly	GTG Val AGG Arg 30 AAG Lys ATA Ile	CTC Leu 15 CAT His TAC Tyr	TGC Cys ACC Thr CCT Pro ATT Ile	et Pl 1 GTG Val CCC Pro TAC Tyr CCA Pro 65	TTG Leu TTC Phe AAA Lys 50 TTC Phe	CTG Leu CAA Gln 35 GAA Glu AGT Ser	GCT Ala 20 CGA Arg GAC Asp ATT Ile	401 449 497 545
74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95	ACG CGG Thr Arg 5 GGA TTG Gly Leu GGA GTA Gly Val ACC ATA Thr Ile	CTG Leu CCT Pro TTC Phe CCT Pro 55	CCG Pro TTT Phe TGT Cys 40 TAT Tyr	TAC Tyr GCA Ala 25 AAT Asn GCG Ala	GTG Val 10 ATT Ile GAT Asp TTA Leu	GCC Ala CTT Leu GAG Glu TTA Leu GAA Glu	CTC Leu ACT Thr TCC Ser GGT Gly 60	GAT Asp TCA Ser ATC Ile 45 GGA Gly	GTG Val AGG Arg 30 AAG Lys ATA Ile	CTC Leu 15 CAT His TAC Tyr	TGC Cys ACC Thr CCT Pro ATT Ile	et Pl 1 GTG Val CCC Pro TAC Tyr CCA Pro 65	TTG Leu TTC Phe AAA Lys 50 TTC Phe	CTG Leu CAA Gln 35 GAA Glu AGT Ser	GCT Ala 20 CGA Arg GAC Asp ATT Ile	401 449 497 545
74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93	ACG CGG Thr Arg 5 GGA TTG Gly Leu GGA GTA Gly Val ACC ATA Thr Ile ATC GTT Ile Val	CTG Leu CCT Pro TTC Phe CCT Pro 55	CCG Pro TTT Phe TGT Cys 40 TAT Tyr	TAC Tyr GCA Ala 25 AAT Asn GCG Ala CTT Leu	GTG Val 10 ATT Ile GAT Asp TTA Leu GGA Gly	GCC Ala CTT Leu GAG Glu TTA Leu GAA Glu 75	CTC Leu ACT Thr TCC Ser GGT Gly 60 ACC Thr	GAT Asp TCA Ser ATC Ile 45 GGA Gly CTG Leu	GTG Val AGG Arg 30 AAG Lys ATA Ile	CTC Leu 15 CAT His TAC Tyr ATC Ile	TGC Cys ACC Thr CCT Pro ATT Ile TAC Tyr 80	GTG Val CCC Pro TAC Tyr CCA Pro 65	TTG Leu TTC Phe AAA Lys 50 TTC Phe	CTG Leu CAA Gln 35 GAA Glu AGT Ser	GCT Ala 20 CGA Arg GAC Asp ATT Ile	401 449 497 545
74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96	ACG CGG Thr Arg 5 GGA TTG Gly Leu GGA GTA Gly Val ACC ATA Thr Ile ATC GTT Ile Val 70 CAC TCA	CTG Leu CCT Pro TTC Phe CCT Pro 55	CCG Pro TTT Phe TGT Cys 40 TAT Tyr	TAC Tyr GCA Ala 25 AAT Asn GCG Ala CTT Leu	GTG Val 10 ATT Ile GAT Asp TTA Leu GGA Gly	GCC Ala CTT Leu GAG Glu TTA Leu GAA Glu 75	CTC Leu ACT Thr TCC Ser GGT Gly 60 ACC Thr	GAT Asp TCA Ser ATC Ile 45 GGA Gly CTG Leu	GTG Val AGG Arg 30 AAG Lys ATA Ile TCT Ser	CTC Leu 15 CAT His TAC Tyr ATC Ile GTT Val	TGC Cys ACC Thr CCT Pro ATT Ile TAC Tyr 80	et Pi 1 GTG Val CCC Pro TAC Tyr CCA Pro 65 TGT Cys	TTG Leu TTC Phe AAA Lys 50 TTC Phe AAC ASn	CTG Leu CAA Gln 35 GAA Glu AGT Ser CTT Leu	GCT Ala 20 CGA Arg GAC Asp ATT Ile TTG- Leu	401 449 497 545
74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 90 91 92 93 94 95 96 97	ACG CGG Thr Arg 5 GGA TTG Gly Leu GGA GTA Gly Val ACC ATA Thr Ile ATC GTT Ile Val 70	CTG Leu CCT Pro TTC Phe CCT Pro 55	CCG Pro TTT Phe TGT Cys 40 TAT Tyr	TAC Tyr GCA Ala 25 AAT Asn GCG Ala CTT Leu	GTG Val 10 ATT Ile GAT Asp TTA Leu GGA Gly	GCC Ala CTT Leu GAG Glu TTA Leu GAA Glu 75	CTC Leu ACT Thr TCC Ser GGT Gly 60 ACC Thr	GAT Asp TCA Ser ATC Ile 45 GGA Gly CTG Leu	GTG Val AGG Arg 30 AAG Lys ATA Ile TCT Ser	CTC Leu 15 CAT His TAC Tyr ATC Ile GTT Val	TGC Cys ACC Thr CCT Pro ATT Ile TAC Tyr 80	et Pi 1 GTG Val CCC Pro TAC Tyr CCA Pro 65 TGT Cys	TTG Leu TTC Phe AAA Lys 50 TTC Phe AAC ASn	CTG Leu CAA Gln 35 GAA Glu AGT Ser CTT Leu	GCT Ala 20 CGA Arg GAC Asp ATT Ile TTG- Leu	401 449 497 545

RAW SEQUENCE LISTING PATENT APPLICATION US/08/842,827

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111			135					140					145				
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113						CGA											833
114	Glu	Tyr	Tyr	Ile	Cys	Arg	Cly	Asn	Ala	Glu	Arg	Val	Lys	Glu	Gly	Arg	
115		150					155					160					
116																	
117	TTG	TCC	TTC	TAT	TCA	GGC	CAC	TCT	TCG	TTT	TCC	ATG	TAC	TGC	ATG	CTG	881
118	Leu	Ser	Phe	Tyr	Ser	Gly	His	Ser	Ser	Phe	Ser	Met	Tyr	Cys	Met	Leu	
119	165			_		170					175		_	_		180	
120																	
121	TTT	GTG	GCA	CTT	TAT	CTT	CAA	GCC	AGG	ATG	AAG	GGA	GAC	TGG	GCA	AGA	929
122	Phe	Val	Ala	Leu	Tvr	Leu	Gln	Ala	Arq	Met	Lvs	Gly	Asp	Trp	Ala	Arg	
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130	Val	GIA		Ser	Arg	Val	ser	_	TYL	ьуз	птэ	HIS		Ser	АБР	Val	
131			215					220					225				
132						a.a	993	aam	ama	amm	993		mm s	amm	aam	am.	1072
133						CAG											1073
134	Leu		GTĀ	Leu	тте	Gln		ата	Leu	vaı	АТа		Leu	val	Ата	val	
135		230					235					240					
136																	
137						TTC											1121
138	Tyr	Val	Ser	Asp	Phe	Phe	Lys	Glu	Arg	Thr		Phe	Lys	Glu	Arg	-	
139	245					250					255					260	
140																	
141	GAG	GAG	GAC	TCT	CAT	ACA	ACT	CTG	CAT	GAA	ACA	CCA	ACA	ACT	GGG	AAT	1169
142	Glu	Glu	Asp	Ser	His	Thr	Thr	Leu	His	Glu	Thr	Pro	Thr	Thr	Gly	Asn	
143					265					270					275		
144																	
145	CAC	TAT	CCG	AGC	AAT	CAC	CAG	CCT	TGA	AAGG	CAG	CAGG	GTGC(C A	GTG!	AAGCT	1223
146	His	Tyr	Pro	Ser	Asn	His	Gln	Pro									
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149	GGC	CTGT	rtt (CTAA	AGGAZ	AA A	rgat'	rgcci	A CA	AGGC	ABA	GGA'	rgca:	rct :	rtct?	CCTGG	1283
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151	TGT	ACAA	CC '	rtta <i>i</i>	AAGA	CT TO	CTGC	rgere	TA E	ATGC	CTCT	TGG	ATGC	ACA (тттс	TGTGT	1343
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RAW SEQUENCE LISTING PATENT APPLICATION US/08/842,827 INPL

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155	AGC	CTTC	CAC (CAAA	ACAG'	rg c	CCCA	CCTG	r at	ACAT!	TTTT	ATT	AAAA	AA	TOTA	ATGCTT	1463
156												ů,		والما			
157	ATG:	[ATA]	AAC A	ATGT	ATGT	AA T	ATGC'	rttci	r AT	TAAE	BATG	TTTC	TTTAE	'AA	ATATA	AATACA	1523
158													٠,			• •	
159	TAT	LAAA 1	ATG :	ratg(GAG	AA C	CAAA	AAAA	A AA	AAAA	AAAA						1563
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165				•	•		: 284			acid	3						
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179	PIO	Pne		Arg	GLY	νат	Pne	40	ASN	Asp	GIU	Ser	Ile 45	гуѕ	Tyt	PIO	
180 181			35					40					43				
182	Trans.	T we	alu	Acn	Пhr	тЪ	Dro	III tare	λla	Lan	F.611	വിയ	Gly	Tla	Tlo	T16	
183	TÀT	50	GIU	кар	1111	116	55	ı yı	ита	Leu	пец	60	GL y	116	116	116	
184		30					"					•					
185	Pro	Phe	Ser	Tle	Tle	Val	Tle	Tle	Leu	Glv	Glu	Thr	Leu	Ser	Val	Tvr	
186	65					70				2	75					80	
187	•					. •											
188	Cvs	Asn	Leu	Leu	His	Ser	Asn	Ser	Phe	Ile	Arq	Asn	Asn	Tyr	Ile	Ala	
189	- 1	•			85					90	•			-	95		
190																	
191	Thr	Ile	Tyr	Lys	Ala	Ile	Gly	Thr	Phe	Leu	Phe	Gly	Ala	Ala	Ala	Ser	
192			•	100			•		105			-		110			
193																	
194	Gln	Ser	Leu	Thr	Asp	Ile	Ala	Lys	Tyr	Ser	Ile	Gly	Arg	Leu	Arg	Pro	
195			115					120					125				
196																	
197	His	Phe	Leu	Asp	Val	Cys	Asp	Pro	Asp	Trp	ser	Lys	Ile	Asn	Cys	Ser	
198		130					135					140					
199		•	•	•													
200	Asp	Gly	Tyr	Ile	Glu	Tyr	Tyr	Ile	Cys	Arg	Gly	Asn	Ala	Glu	Arg		
201	145	4				150					155					160	
202		_:					_			_							
203	Lys	Gla	Gly,	Arg		Ser	Phe	Tyr	Ser	_	His	Ser	Ser	Phe		Met	
204		4			165					170					175		

RAW SEQUENCE LISTING PATENT APPLICATION US/08/842,827

DATE: 09/11/97 TIME: 11:39:27

INPUT SET: S20239.raw Cys Met Leu Phe Val Ala Leu Tyr Leu Gln Ala Arg Met Lys Gly Asp Trp Ala Arg Leu Leu Arg Pro Thr Leu Gln Phe Gly Leu Val Ala 25.4.45.4.7 Val Ser Ile Tyr Val Gly Leu Ser Arq Val Ser Asp Tyr Lys His His Trp Ser Asp Val Leu Thr Gly Leu Ile Gln Gly Ala Leu Val Ala Ile Leu Val Ala Val Tyr Val Ser Asp Phe Phe Lys Glu Arg Thr Ser Phe Lys Glu Arg Lys Glu Glu Asp Ser His Thr Thr Leu His Glu Thr Pro Thr Thr Gly Asn His Tyr Pro Ser Asn His Gln Pro (2) INFORMATION FOR SEQ ID NO:3: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1566 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 342..1196 (ix) FEATURE: (A) NAME/KEY: mat peptide (B) LOCATION: 342..1196 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3: CCTGTGGGAG AGAGCGCCGG GATCCGGACG GGGTAGCAAC CGGGGCAGGC CGTGCCGGCT GAGGAGGTCC TGAGGCTACA GAGCTGCCGC GGCTGGCACA CGAGCGCCTC GGCACTAACC GAGTGTTCGC GGGGCTGTG AGGGGAGGGC CCCGGGCGCC ATTGCTGGCG GTGGGAGCGC > CGCCCGGTCT CAGCCCGCCC TCGCCTGCTC TCCTCCTCCG GCTGGGAGGG GCCGTATCTC GGGGCCGTCG CCAGCCCCGG CCCGGGCTCG ATAATCAAGG GCCTCGGCCG TCGTCQCGCA . CCTCATTCCA TCGCCCTTGC CGGGCAGCCC GGGCAGAGAC C ATG TTT GAC AAG PAGÉ: 1

SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/08/842,827

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